

SEQUENCE LISTING

<110> Ruben et al.

<120> Human Tumor Necrosis Factor Receptor TR17

<130> PF524P1

<140> Unassigned

<141> 2001-09-25

<150> 60/254,874

<151> 2000-12-13

<150> 60/235,991

<151> 2000-09-26

<150> 09/533,822

<151> 2000-03-24

<150> 60/188,208

<151> 2000-03-10

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 882

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(882)

<400> 1

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Met	Ser	Gly	Leu	Gly	Arg	Ser	Arg	Arg	Gly	Gly	Arg	Ser	Arg	Val	Asp	
1				5					10					15		

cag	gag	gag	cgc	ttt	cca	cag	ggc	ctg	tgg	acg	ggg	gtg	gct	atg	aga	96
Gln	Glu	Glu	Arg	Phe	Pro	Gln	Gly	Leu	Trp	Thr	Gly	Val	Ala	Met	Arg	
		20						25					30			

tcc	tgc	ccc	gaa	gag	cag	tac	tgg	gat	cct	ctg	ctg	ggg	acc	tgc	atg	144
Ser	Cys	Pro	Glu	Glu	Gln	Tyr	Trp	Asp	Pro	Leu	Leu	Gly	Thr	Cys	Met	
		35					40					45				

tcc	tgc	aaa	acc	att	tgc	aac	cat	cag	agc	cag	cgc	acc	tgt	gca	gcc	192
Ser	Cys	Lys	Thr	Ile	Cys	Asn	His	Gln	Ser	Gln	Arg	Thr	Cys	Ala	Ala	
		50				55					60					

ttc	tgc	agg	tca	ctc	agc	tgc	cgc	aag	gag	caa	ggc	aag	ttc	tat	gac	240
Phe	Cys	Arg	Ser	Leu	Ser	Cys	Arg	Lys	Glu	Gln	Gly	Lys	Phe	Tyr	Asp	
65						70				75				80		

cat	ctc	ctg	agg	gac	tgc	atc	agc	tgt	gcc	tcc	atc	tgt	gga	cag	cac	288
His	Leu	Leu	Arg	Asp	Cys	Ile	Ser	Cys	Ala	Ser	Ile	Cys	Gly	Gln	His	
				85					90				95			

cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc cca gtg 336
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110

aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt gaa aac 384
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125

aat tca gac aac tgc gga agg tac caa gga ttg gag cac aga ggc tca 432
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140

gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat cag gtg 480
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160

gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc gtc ctc tgc 528
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
 165 170 175

tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag agg ggg gat ccc 576
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
 180 185 190

tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg gcc aag tct 624
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
 195 200 205

tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg agc aca tcc ccc 672
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
 210 215 220

gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc agg gcg ccc 720
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
 225 230 235 240

acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc act tgt gct 768
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
 245 250 255

gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag cct tgc cca 816
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
 260 265 270

cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct gcc cag gag 864
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
 275 280 285

ggg ggc cca ggt gca taa 882
 Gly Gly Pro Gly Ala
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<211> 293

<212> PRT

<213> Homo sapiens

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 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
 35 40 45
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50 55 60
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65 70 75 80
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85 90 95
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100 105 110
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115 120 125
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130 135 140
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145 150 155 160
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
 165 170 175
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
 180 185 190
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
 195 200 205
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
 210 215 220
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
 225 230 235 240
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Thr Pro Asp Pro Thr Cys Ala
 245 250 255
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
 260 265 270
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
 275 280 285
 Gly Gly Pro Gly Ala
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<210> 3

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<212> DNA

<213> Homo sapiens

<400> 3

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 tctctcgggac tcttgaggtc acatgcgtgg ttggtggagct aagccacgaa gacctgagg 180
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcatata tgccaagaca aagccgcggg 240
 agggagcagta caacagcacg tacogtgtgg tcagcgtctct caccgtctctg caccaggact 300
 ggctgaatgg caaggagtag aagtgcgaag tctccaacaa agccctccca acccccatcg 360
 agaaaaacct ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgctctgtc aaaggcttct 480
 atccaagcga catcgccgtg gaggtaggaga gcaatgggca gccggagaa aactacaaga 540
 ccacgcctcc cgtgctggac tccgacggct ccttctctct ctacagcaag ctcaccgtgg 600
 acaagagcag gtggcagcag gggaaagtct tctcatgtct cgtgatgatc gaggctctgc 660
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 gactctagag gat 733

<210> 4
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)..(5)
<223> Xaa equal any amino acid

<220>
<221> SITE
<222> (9)
<223> Xaa equal any amino acid

<400> 4
Xaa Xaa Xaa Xaa Xaa Glu Gly Ser Xaa
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<210> 5
<211> 9
<212> PRT
<213> Homo sapiens

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<221> SITE
<222> (3)
<223> Xaa equal is any amino acid

<400> 5
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<210> 6
<211> 17
<212> PRT
<213> Homo Sapiens

<400> 6
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Ala

<210> 7
<211> 22
<212> PRT
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<221> SIGNAL
<222> (1)..(22)
<223> consensus signal sequence

<400> 7

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Trp	Ala	Pro	Ala	Arg	Gly
			20		

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